

FIGURE 1A

Organism ID	Di-potassium EDTA		Di-ammonium EDTA		Di-sodium EDTA		Tri- sodium EDTA		Tetra-sodium EDTA	
	MIC	MBC	MIC	MBC	MIC	MBC	MIC	MBC	MIC	MBC
S24 Staph. epidermidis	<0.5	8	<0.5	4	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5
31 Staph. epidermidis	<0.5	8	<0.5	8	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5
301 Staph. xylosus	<0.5	6	<0.5	4	<0.5	<0.5	<0.5	<0.5	<0.5	20
300 Staph. capitis	<0.5	10	<0.5	8	<0.5	<0.5	<0.5	<0.5	<0.5	10
J46 Staph. lentus	<0.5	10	<0.5	10	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5
S24 Staph. capitis	<0.5	8	<0.5	10	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5
R8 Staph. simulans	<0.5	8	<0.5	10	<0.5	1	<0.5	1.5	<0.5	1
72 S. aureus	1	6	1	6	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5
R57 S. aureus	1	8	1	10	<0.5	10	<0.5	<0.5	<0.5	8
R13 S. aureus	1	6	1	15	<0.5	10	<0.5	<0.5	<0.5	<0.5
R30 S. aureus	1	8	1	15	<0.5	10	<0.5	<0.5	-----	-----
8 S. aureus	1	8	1	10	<0.5	<0.5	<0.5	<0.5	-----	-----
R64 MRSA	1	6	1	8	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5

FIGURE 1B

Organism ID	Di-potassium EDTA		Di-ammonium EDTA		Di-sodium EDTA		Tri- sodium EDTA		Tetra-sodium EDTA	
	MIC	MBC	MIC	MBC	MIC	MBC	MIC	MBC	MIC	MBC
R51 MRSA	1	10	1	6	<0.5	1	<0.5	<0.5	<0.5	<0.5
R92 MRSA	1	8	1	>15	<0.5	10	<0.5	<0.5	<0.5	<0.5
S93 MRSA	1	8	1	10	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5
J67 MRSA	1	8	1	10	<0.5	10	<0.5	<0.5	<0.5	<0.5
R8 VRE	<0.5	8	<0.5	15	<0.5	100	<0.5	20	<0.5	30
Woods VRE	1	8	1	>15	<0.5	100	<0.5	2	<0.5	1
S77 Enterococcus Faecium	<0.5	8	<0.5	15	<0.5	100	<0.5	20	<0.5	6
S76 Enterococcus faecalis	1	15	1	15	<0.5	100	<0.5	1.5	<0.5	40
68 Klebsiella pneumoniae	1.5	15	4	>10	8	60	20	40	6	6
R51 Klebsiella pneumoniae	1	15	1.5	>10	-----	-----	-----	-----	-----	-----
128 Klebsiella oxytoca	1	15	1	>10	1	90	4	20	4	6
J7 Klebsiella ornitholytica	1	>15	1	>10	1	60	20	70	4	8
250 E. coli	1	>15	1	>10	1.5	80	10	20	1.5	1.5
B/C E. coli	1	15	1.5	>10	-----	-----	-----	-----	-----	-----

FIGURE 1C

Organism ID	Di-potassium EDTA		Di-ammonium EDTA		Di-sodium EDTA		Tri- sodium EDTA		Tetra-sodium EDTA	
	MIC	MBC	MIC	MBC	MIC	MBC	MIC	MBC	MIC	MBC
137 E. coli	1	15	4	>10	4	60	4	10	2	2
292 Ent. cloacae	4	15	4	>10	4	>100	20	20	6	15
190 Ent. cloacae	4	>15	4	>10	4	100	20	20	6	15
J22 Ent. cloacae	6	>15	<0.5	>10	6	>100	20	20	6	10
R4 Steno. maltophilia	<0.5	10	1	>10	-----	-----	-----	-----	-----	-----
B/C Pseudomonas aeruginosa	1	>15	1	>10	-----	-----	-----	-----	-----	-----
J20 Pseudomonas aeruginosa	1	>15	1	>10	<0.5	50	4	20	2	4
J26 Pseudomonas sp.	1	15	<0.5	>10	<0.5	25	4	60	8	4
R75 Coryne. amycolatum	<0.5	<0.5	<0.5	1	NG	NG	NG	NG	<0.5	20
R23 Coryne. strait/amy	<0.5	<0.5	<0.5	1	NG	NG	NG	NG	<0.5	<0.5
177 Acinetobacter baumannii	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5
J44 Acinetobacter baumannii	<0.5	60-70	<0.5	>10	<0.5	1	<0.5	<0.5	<0.5	<0.5

FIGURE 1D

Organism ID	Di-potassium EDTA		Di-ammonium EDTA		Di-sodium EDTA		Tri- sodium EDTA		Tetra-sodium EDTA	
	MIC	MBC	MIC	MBC	MIC	MBC	MIC	MBC	MIC	MBC
R16 Proteus mirabilis	<0.5	>15	<0.5	>10	<0.5	50	<0.5	40	<0.5	15
R81 Proteus vulgaris	1	>15	<0.5	>10	<0.5	15	<0.5	40	<0.5	8
R26 Proteus mirabilis	<0.5	15	<0.5	>10	<0.5	50	<0.5	60	1	15

FIGURE 2

Organism ID	Tetra-sodium MIC	Tetra-sodium MBC	Di-potassium MIC	Di-potassium MBC	Di-ammonium MIC	Di-ammonium MBC
J96 Candida albicans	0.5	15	0.5	>100	0.5	>100
J92 Candida albicans	0.5	15	0.5	>100	0.5	>100
Myc. Candida albicans	0.5	0.5	0.5	>100	0.5	>100
J98 Candida lucitaniae	0.5	6	0.5	>100	0.5	>100
Myc. Candida tropicalis	0.5	10	1	>100	1	100
Myc. Candida Guilliermondii	0.5	0.5	0.5	>100	0.5	>100
Myc. Candida glabrata	0.5	2	0.5	>100	0.5	90
Myc. Candida parapsilosis	0.5	8	0.5	>100	0.5	100
J96 Candida glabrata	0.5	8	0	100	0.5	>100

FIGURE 3A

Organism ID	Cupric Di-sodium EDTA		Magnesium Di-sodium EDTA		Ferric sodium EDTA	
	MIC	MBC	MIC	MBC	MIC	MBC
S24 Staph. epidermidis	<0.5	<0.5	6	30	>20	>30
31 Staph. epidermidis	<0.5	<0.5	6	30	>20	>30
301 Staph. xylosum	<0.5	<0.5	2	>30	>20	>30
300 Staph. capitis	<0.5	<0.5	1.5	>30	>20	>30
J46 Staph. lentus	<0.5	<0.5	6	>30	>20	>30
S24 Staph. capitis	<0.5	<0.5	6	>30	>20	>30
R8 Staph. simulans	<0.5	<0.5	1.5	>30	>20	>30
72 S.aureus	<0.5	<0.5	>30	>30	>20	>30
R57 S.aureus	<0.5	<0.5	>30	>30	>20	>30
R13 S.aureus	<0.5	<0.5	>30	>30	>20	>30
R30 S.aureus	<0.5	<0.5	>30	>30	>20	>30
8 S.aureus	<0.5	<0.5	>30	>30	>20	>30
R64 MRSA	<0.5	<0.5	>30	>30	>20	>30
R51 MRSA	<0.5	<0.5	>30	>30	>20	>30
R92 MRSA	<0.5	<0.5	>30	>30	>20	>30
S93 MRSA	<0.5	<0.5	>30	>30	>20	>30
J67 MRSA	<0.5	<0.5	>30	>30	>20	>30
R8 VRE	<0.5	<0.5	25	>30	2	>30
Woods VRE	>30	>30	>30	>30	>20	>30
S77 Enterococcus faecium	<0.5	<0.5	1.5	>30	4	>30
S76 Enterococcus faecalis	<0.5	<0.5	>30	>30	4	>30
68 Klebsiella pneumoniae	>30	>30	>30	>30	>15	>15
R51 Klebsiella pneumoniae	>30	>30	>30	>30	15	>15

FIGURE 3B

Organism ID	Cupric Di-sodium EDTA		Magnesium Di-sodium EDTA		Ferric sodium EDTA	
	MIC	MBC	MIC	MBC	MIC	MBC
128 Klebsiella oxytoca	>30	>30	>30	>30	>15	>15
J7 Klebsiella ornitholytica	>30	>30	>30	>30	15	>15
250 E. coli	>30	>30	>30	>30	15	>15
B/C E. coli	6	>30	>30	>30	>15	>15
137 E. coli	>30	>30	>30	>30	>15	>15
292 Ent. cloacae	>30	>30	>30	>30	>15	>15
190 Ent. cloacae	>30	>30	>30	>30	>15	>15
J22 Ent. cloacae	6	8	>30	>30	10	>15
R4 Steno. maltophilia	6	>30	>30	>30	15	>15
B/C Pseudomonas aeruginosa	>30	>30	>30	>30	15	>15
J20 Pseudomonas aeruginosa	>30	>30	>30	>30	15	>15
J26 Pseudomonas sp.	>30	>30	>30	4	10	10
R75 Coryne. amycolatium	<0.5	<0.5	<0.5	4	10	10
R23 Coryne. strait/amy	<0.5	<0.5	<0.5	<0.5	6	10
177 Acinetobacter baumannii	<0.5	<0.5	<0.5	<0.5	>15	>15
J44 Acinetobacter baumannii	6	15	>30	>30	>15	>15
R16 Proteus mirabilis	6	>30	>30	.30	>15	>15
R81 Proteus vulgaris	>30	>30	>30	>30	>15	>15
R26 Proteus mirabilis	6	>30	>30	>30	>15	>15

FIGURE 4A

Organism ID	Cupric Di-sodium+ tetrasodium EDTA			Cupric Di-sodium + Di-potassium EDTA		Cupric Di-sodium + Di-ammonium EDTA	
	MIC	MBC		MIC	MBC	MIC	MBC
S24 Staph. epidermidis	0.25	2		0.25	15	0.5	20
31 Staph. epidermidis	0.25	8		0.25	20	0.5	20
301 Staph. xylosus	<0.1	>20		<0.1	>20	<0.1	20
300 Staph. capitis	<0.1	>20		<0.1	20	<0.1	20
J46 Staph. lentus	0.25	6		0.25	15	0.5	20
S24 Staph. capitis	0.25	8		0.25	20	0.5	20
R8 Staph. simulans	0.25	>20		1	>20	1	20
72 S.aureus	<0.1	>20		<0.1	>20	<0.1	20
R57 S.aureus	<0.1	>20		<0.1	20	<0.1	20
R13 S.aureus	<0.1	>20		<0.1	20	<0.1	>20
R30 S.aureus	<0.1	15		<0.1	20	<0.1	>20
8 S.aureus	<0.1	>20		<0.1	>20	<0.1	20
R64 MRSA	<0.1	>20		<0.1	>20	<0.1	>20
R51 MRSA	<0.1	>20		<0.1	20	<0.1	>20

FIGURE 4B

Organism ID	Cupric Di-sodium + tetrasodium EDTA		Cupric Di-sodium + Di-potassium EDTA		Cupric Di-sodium + Di-ammonium EDTA	
	MIC	MBC	MIC	MBC	MIC	MBC
R92 MRSA	<0.1	>20	<0.1	>20	<0.1	>20
S93 MRSA	<0.1	15	<0.1	20	<0.1	20
J67 MRSA	<0.1	>20	<0.1	20	<0.1	20
R8 VRE	0.25	20	0.25	20	0.5	>20
Woods VRE	0.25	>20	<0.1	20	<0.1	>20
S77 Enterococcus faecium	0.5	>20	0.5	>20	1	>20
S76 Enterococcus faecalis	0.25	>20	<0.1	>20	<0.1	>20
68 Klebsiella pneumoniae	10	>20	6	>20	2	>20
R51 Klebsiella pneumoniae	4	>20	4	>20	2	>20
128 Klebsiella oxytoca	4	>20	2	>20	2	>20
J7 Klebsiella ornitholytica	6	>20	2	>20	2	>20
250 E. coli	6	15	2	>20	2	>20
B/C E. coli	6	1	2	>20	2	>20
137 E. coli	6	4	2	>20	2	>20
292 Ent. cloacae	20	>20	8	>20	8	>20

FIGURE 4C

Organism ID	Di-sodium + tetrasodium EDTA		Cupric Di-sodium + Di-potassium EDTA		Cupric Di-sodium + Di-ammonium EDTA	
	MIC	MBC	MIC	MBC	MIC	MBC
190 Ent. cloacae	20	>20	8	>20	6	>20
J22 Ent. cloacae	20	>20	8	>20	6	>20
R4 Steno. maltophilia	6	10	1	>20	1	>20
B/C Pseudo-monas aeruginosa	6	10	2	>20	2	>20
J20 Pseudo-monas aeruginosa	6	15	2	>20	2	>20
J26 Pseudo-monas sp.	6	>20	2	>20	2	>20
R75 Coryne. amycolatium	<0.1	<0.1	0.25	0.25	0.25	0.25
R23 Coryne. strait/amy	6	10	1	>20	1	>20
177 Acineto-bacter baumannii	6	0.5	0.5	0.25	0.25	<0.1
J44 A. baumannii	6	>20	2	>20	1	>20
R16 Proteus mirabilis	6	>20	2	>20	1	>20
R81 Proteus vulgaris	6	>20	2	>20	2	>20
R26 Proteus mirabilis	6	>20	2	>20	1	>20

FIGURE 5A

Organism ID	Tetrasodium + Di-ammonium EDTA		Tetrasodium + Di-potassium EDTA		Di- ammonium + Di- potassium EDTA	
	MIC	MBC	MIC	MBC	MIC	MBC
S24 Staph. epidermidis	0.5	>20	1	20	0.5	>8
31 Staph. epidermidis	0.5	>20	1	6	0.5	>8
301 Staph. xyloso	0.5	>20	1	>20	0.5	>8
300 Staph. capitis	0.5	>20	1	>20	0.5	8
J46 Staph. lentus	0.5	>20	0.5	8	0.5	>8
S24 Staph. capitis	0.5	>20	0.5	8	0.5	>8
R8 Staph. simulans	0.5	>20	0.5	>20	0.5	>8
72 S. aureus	1	>20	0.5	20	0.5	8
R57 S. aureus	1	>20	1	20	1	>8
R13 S. aureus	0	0	0	0	0	0
R30 S. aureus	1	4	1	4	1	8
8 S. aureus	1	>20	1	20	1	8
R64 MRSA	1	>20	1	20	1	>8
R51 MRSA	1	>20	1	20	0.5	>8

FIGURE 5B

Organism ID	Tetrasodium + Di-ammonium EDTA		Tetrasodium + Di-potassium EDTA		Di- ammonium + Di-potassium EDTA	
	MIC	MBC	MIC	MBC	MIC	MBC
R92 MRSA	1	>20	1	>20	1	>8
S93 MRSA	1	>20	1	20	1	8
J67 MRSA	1	>20	1	>20	1	8
R8 VRE	1	>20	1	>20	1	>8
Woods VRE	1	>20	1	>20	1	>8
S77 Enterococcus faecium	0.5	>20	1	>20	1	>8
S76 Enterococcus faecalis	1	>20	1	>20	1	>8
68 Klebsiella pneumoniae	>20	>20	>20	>20	10	>10
R51 Klebsiella pneumoniae	1	>20	1	>20	1	>10
128 Klebsiella oxytoca	1	>20	1	>20	1	>10
J7 Klebsiella ornitholytica	>20	>20	20	>20	10	>10
250 E. coli	>20	>20	20	>20	2	>10
B/C E. coli	1	0.5	1	1	0.5	>10
137 E. coli	4	>20	20	>20	1	>10
292 Ent. cloacae	8	>20	>20	>20	4	>10

FIGURE 5C

Organism ID	Tetrasodium + Di-ammonium EDTA		Tetrasodium + Di-potassium EDTA		Di- ammonium + Di- potassium EDTA	
	MIC	MBC	MIC	MBC	MIC	MBC
190 Ent. cloacae	>20	>20	>20	>20	6	>10
J22 Ent. cloacae	>20	>20	>20	>20	4	>10
R4 Steno. maltophilia	1	>20	1	>20	0.5	>10
B/C Pseudo-monas aeruginosa	8	>20	15	15	2	>10
J20 Pseudo-monas aeruginosa	6	>20	15	20	2	>10
J26 Pseudo-monas sp.	8	>20	20	>20	2	>10
R75 Coryne. amycolatum	0.5	4	0.5	1	0.5	2
R23 Coryne. strait/amy	0.5	0.5	0.5	0.5	0.5	0.5
177 Acinetobacter baumannii	4	8	1	>20	0.5	>10
J44 A. baumannii	>20	>20	>20	>20	2	>10
R16 Proteus mirabilis	1	>20	1	>20	0.5	>10
R81 Proteus vulgaris	1	>20	1	>20	0.5	>10
R26 Proteus mirabilis	>20	>20	>20	>20	2	>10

FIGURE 6

Organism	Tetra-sodium EDTA MBEC (mg/ml, w/v)
31 Staph. epidermidis	20-40
301 Staph. xylosus	20-40
300 Staph. capitis	<5
J46 Staph. lentus	<5
R8 Staph. simulans	20-40
72 Staph. aureus	<5
R57 Staph. aureus	<5
8 Staph. aureus	<5
R92 MRSA	<5
S93 MRSA	<5
J67 MRSA	<5
68 Klebsiella pneumoniae	<5
J7 Klebsiella ornitholytica	<5
292 Enterobacter cloacae	20
190 Enterobacter cloacae	15
J22 Enterobacter cloacae	<20
R4 Stenotrophomonas maltophilia	<10
J20 Pseudomonas aeruginosa	<5
J26 Pseudomonas aeruginosa	10
J44 Acinetobacter baumannii	<5
R16 Proteus mirabilis	<5
R81 Proteus vulgaris	<5
H Enterococcus	<5
7097651 E. coli	<10
250 E. coli	<5
7115649 Klebsiella oxytoca	<5

FIGURE 7

Catheter ID	EDTA Conc. (mg/mL)	Colony count at 0 hours (cfu/mL)	Colony count at 3 hours (cfu/mL)	Colony count at 6 hours (cfu/mL)	Colony count at 24 hours (cfu/mL)	Organisms Present
G	40	>100000	120000	6000	0	Mixed Gram-ve and Gram+ve cultures
H	40	>100000	80000	0	0	Mixed Gram-ve and Gram+ve cultures
I	40	200000	>500000	25000	0	CNS + Coryneforms
J	40	>500000	180000	0	0	CNS
K	40	>1000000	600000	500000	180000	Streptococcus sp., CNS and Gram-ve bacillus
P	40	>500000	2500000	150000	54500	Pseudomonas sp. + Streptococcus sp.
Q	40	205000	650000	1000	5500	Enterococcus sp.
R	40	5000	500	0	0	MRSA
S	40	>500000	100000	30000	0	CNS
T	40	137500	1000	0	0	MRSA
U	40	>500000	182500	67500	13500	CNS
V	40	700000	38500	37500	13000	CNS + Group D Streptococcus
W	40	>500000	0	0	0	Enterobacter cloacae
X	40	>500000	20000	0	0	Mixed CNS
Z	40	>500000	0	0	0	CNS
A1	40	700000	37000	60000	0	MRSA
B1	40	24000	0	0	0	MRSA

FIGURE 8

Catheter ID	EDTA Conc. (mg/mL)	Colony count at 0 hours (cfu/mL)	Colony count at 3 hours (cfu/mL)	Colony count at 6 hours (cfu/mL)	Colony count at 24 hours (cfu/mL)	Organisms Present
A	100	1000000	0	0	0	CNS
B	100	1000000	100	200	0	CNS
C	50	1000000	0	0	0	Mixed coliforms
D	20	>100000	250000	100000	0	Mixed Gram-ve and Gram+ve cultures
E	30	>100000	400000	360000	0	Mixed Gram-ve and Gram+ve cultures
F	30	300000	57000	2000	0	Mixed Gram-ve and Gram+ve cultures
L	60	600000	5000	4000	0	Enterococcus sp.
M	60	>500000	300000	17000	17000	Proteus sp. and CNS
O	50	500000	30000	130000	0	Staphylococcus aureus
N (arterial)	50	500000	10000	0	0	CNS
N (venous)	50	300000	10000 (CNS only)	60000 (CNS only)	0	Klebsiella pneumoniae + CNS